```
C; Keywords: transcription regulation
                                                                                                                                           R:Park J.S.; Luethy J.D.; Wang, M.G.; Fargnoli, J.; Fornace Jr., A.J.; McBride, O.W.; Gene 116, 259-267, 1992
A:Title: Tsolation; Characterization and chromosomal localization of the human GADD153.
A:Reference number: JC1169; MUID:92339899
A:Accession: JC1169
                                                                                                          A; Molecule type: mRNA
A; Residues: 1-168 < PAR>
                                                                                                                                                                                                                                                                                                                                                       RESULT
JC1169
                                   A; Gene: GADD153
                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 05-Mar-1993 #sequence_reviside 05-Mar-1993 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 12q13/16p1
A; Note: TLS is a synonym f
C; Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: EMBL:X71427; NID:g395919; PIDN:CAA50558.1; PID:g4210364 C;Comment: This sequence is the chimeric product of a translocation mutation C;Genetics:
A:Gene: GADD153/FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 38-Nov-1995 #:
C:Accession: S33798; S36158
                                                                                                                                                                                                                                                            C:Accession: JC1169
                                                                                                                                                                                                                                                                                                                        DNA-damage-inducible protein GADD153 - h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-462 < RAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Fusion of the deminant negative transcription regulator CHOP with a novel A;Reference number: S36157; MUID:93350637 \Lambda;Accession: S36158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S62138; NID:g386258; PIDN:AAB27103.1; PID:g386159 R;Rabbitts, T.H.; Forster, A.; Larson, R.; Nathan, P. Nature Genet. 4, 175-180, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-462 <CRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Title: Fusion of CHOP to a novel RNA-binding profein in human myxoid liposarcoma. A:Reference number: S33798; MUID:93288139
A:Accession: S33798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Crozat, A.; Aman, P.; Mandahl, N., Ron, D. Nature 363, 640-644, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUS/CHOP mutant fusion protein - human N:Alternate names: TLS/CHOP mutant fusion protein
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                                                                      Comment: This protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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Map position: 12q13/16p11
Note: TLS is a synonym fo
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                                                                                                                                                                                                                                                                                                                                                                                                                              354 AWLTEEEPEPAEVTSTSQSPHSPDSSQSSLAQEEEEEDQG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 MAAESLPFSFGTLSSWELEAWYEDLQEVLSSDENGGTYVSPPGNEEEESKIFTTLDPASL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AWLT-EEPGPTEVTRTSQSPRSPDSSQSSMAQEEEEEEQG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAAESLPFTLETVSSWELEAWYEDLQEVLSSDEIGGTYISSPGNEEEESKTFTTLDPASL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAAESLPFTLETVSSWELEAWYEDLQEVLSSDEIGGTYISSPGNEEEESKTFTTLDPASL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAAESLPFTLETVSSWELEAWYEDLQEVLSSDENGGPYSSSLGNEEGESKTFTTLDPASL 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                           GB:S40706; NID:g252001; PIDN:AAB22646.1; tein is responsible for the growth arrest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.7%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDB: FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 430.5; DB 4
Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. N2 ~ M 1. N363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
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                                                                                      PID:g252002
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Matches
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A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A; Accession: F84770
                                                                                               A; Map position:
                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-263 <STO>
                                                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2g35600 [Imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
F84770
                                                                                                                             A; Gene: At2g35600
                                                                                                                                                   C; Genetics:
                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                           A:Status: preliminary
                                                                                                                                                                                                                                                                                                                      A;Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: This protein translocates to the nucleus and directly functions in mitogen F;1-98/Region: hath #status predicted F;155-170/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-237 <IZU>
A; Cross-references: DBBJ: D63707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Izumoto, Y:; Kuroda, T.; Harada, H.; Kishimoto, T.; Nakamura, H. Biochem. Biophys. Res. Commun. 238, 26-32, 1997
A:Title: Hepatoma-derived growth factor belongs to a gene family in mice showing sign A:Reference number: JC5660; MUID:97445118
A:Recession: JC5660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
JC5660
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C;Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: HDGF
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                              Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 SSDEEGKLVIDEPAKEKNEKGTLKRRAGDVLEDSPKRPKESGDHEEEDKEIAALE---- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 --GERPLPVEVEKNS-TPSEPDSGQGPPAEEEEGEEE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 WLTEEPGPTEVTRTSQSPRSPDSSQSSMAQEEEEEEQ 98
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                                                                                                                                                             GB:AE002093; NID:g3608128; PIDN:AAC36161.1; GSPDB:GN00139
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18.5%; Score 94; I
25.8%; Pred. No. 0
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85.0%;
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                 DB 2; Length 263;
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Local Similarity

31;

Conservative

19;

Mismatches

42;

Indels

28;

Gaps

.12;

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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                  508
435
430.5
421
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 PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 Match
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Gapop 10.0 , Gapext 0.5
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508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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S45736
S45736
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T739559
T739564
S69969
S69969
S69969
S69969
S728055
T25186
T25186
T25186
T30250
T40187
T146187
T15827
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TyA protein - yeas
TyA protein - yeas
TyB protein - yeas
probable ubiquinol
hypothetical prote
hypothetical prote
hypothetical protein - yeas
mysoin-like protei
TyB protein - yeas
mysoin-like protei
TyB protein - yeas
hepatoma-derived
TyB protein - yeas
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protein - mous
hepatoma-derived
protein - mous
hypothetical prote
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gas-vesicle operon
hypothetical prote
gas-vesicle operon
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DNA damage inducib
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DNA-damage-inducib
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hypothetical prote
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RESULT 2 A34096 DNA damage inducible protein - Chinese hamster C; Species: Cricetulus griseus (Chinese hamster) C; Species: O4-Apr-1990 #sequence_revision 04-Apr-1990 #text_0 C; Accession: A34096 R; Fornace Jr., A.J.; Nebert, D.W.; Hollander, M.C.; Lueth; Mol. Cell. Biol. 9, 4196-4203, 1989 A; Title: Mammalian genes coordinately regulated by growth A; Reference number: A34096; MUID:90066424 A; Accession: A34096 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-168 <for> A; Cross-references: GB:M29238; NID:g191077; PIDN:AAA36982 C; Keywords: transcription regulation</for>	Query Match Guery Match Best Local Similarity 100.0%; Score 508; DB 2; Length 168; Best Local Similarity 100.0%; Pred. No. 1.7e-41; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 MAAESLPFTLETVSSWELEAWYEDLQEVLSSDEIGGTYISSPGNEEEESKTFTTLDPASL 60 [RESULT 1 \$26148 nuclear protein chop-10 - mouse C;Species: Mus muscullus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_c; C;Accession: \$26148 R;Ron, D.; Habener, J.F. Genes Dev. 6, 439-453, 1992 A;Title: CHOP, a novel developmentally regulated nuclear p A;Reference number: \$26148; MUID:92192456 A;Accession: \$26148 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-168 <rond a;cross-references:="" c;keywords:="" embl:x67083;="" nid:g50406;="" pidn:caa47465="" regulation<="" th="" transcription=""><th>30 73.5 14.5 1114 2 I50222 31 73 14.4 113 2 C89828 32 73 14.4 648 2 H84587 33 72.5 14.3 349 2 T42965 34 72 14.2 617 2 A56051 35 72 14.2 2137 2 T34634 36 72 14.2 2232 2 T34434 37 71.5 14.1 1210 2 I39410 39 71.5 14.1 1210 2 I39410 40 71 14.0 309 2 T00503 41 71 14.0 309 2 T00503 42 71.5 14.1 1217 2 JC4934 43 70.5 13.9 185 2 C70550 44 70.5 13.9 555 2 A56560 45 70.5 13.9 672 2 T12524 ALIGNMENTS</th></rond>	30 73.5 14.5 1114 2 I50222 31 73 14.4 113 2 C89828 32 73 14.4 648 2 H84587 33 72.5 14.3 349 2 T42965 34 72 14.2 617 2 A56051 35 72 14.2 2137 2 T34634 36 72 14.2 2232 2 T34434 37 71.5 14.1 1210 2 I39410 39 71.5 14.1 1210 2 I39410 40 71 14.0 309 2 T00503 41 71 14.0 309 2 T00503 42 71.5 14.1 1217 2 JC4934 43 70.5 13.9 185 2 C70550 44 70.5 13.9 555 2 A56560 45 70.5 13.9 672 2 T12524 ALIGNMENTS
text_change 05-Nov-1999 Luethy, J.D.; Papathanasiou, M.; prowth arrest signals and DNA-dama	Length 168; Indels 0; Gaps 0; EBEBESKTFTTLDPASL 60 [_change 05-Nov-1999 protein that dimerizes with 65.1; PID:950407	deltaEF1 - chicken conserved hypothet probable WD-40 rep glycoprotein - ate myocyte nuclear fa PIP82 protein - fr hypothetical prote chromogranin A pre AF-4 protein, spli serine/proline-ric probable MYB famil probable transcrip delta-crystallin/E hypothetical prote zinc finger protei hypothetical prote hypothetical protein

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SMCY_MOUSE
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FXK1_MOUSE
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AF4_HUMAN
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DDIT3 OR CHOP OR GADD153.
Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Growth arrest and DNA-damage-inducible protein GADD153 (DNA-damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fornace A.J. Jr., Nebert D.W., Hollander M.C., Luethy J.D., Papathanasiou M., Fargnoli J., Holbrook N.J.; "Mammalian genes coordinately regulated by growth arrest signals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: SOME, TO BZIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: INHIBITS THE DNA-BINDING ACTIVITY OF C/EBP AND LAP FORMING HETERODIMERS THAT CANNOT BIND DNA.
-1- FUNCTION: MAY PLAY A ROLE IN THE INHIBITION OF GROWTH AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-damaging agents.";
Mol. Cell. Biol. 9:4196-4203(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90066424; PubMed=2573827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10030;
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GA15_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M29238; AAA36982.1; -.
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                                                                                                                                                       61
                                                                                                                                                                                                             61 AWLTEEPGPTEVTRTSQSPRSPDSSQSSMAQEEEEEE 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA DAMAGE AS WELL AS IN THE MAINTENANCE OF GROWTH ARREST
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                                                                                                                                                                                                                                                                            MAAESLPFTLETVSSWELEAWYEDLQEVLSSDENGGPYSSSLGNEEGESKTFTTLDPASL
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SM00338; BRLZ; 1.
SM00338; Nuclear protein; Transcription regulation;
92 95 POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18831 MW;
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88.7%;
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Pred. No. 1
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      PRT;
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1 MAAESLPFSFGTLSSWELEAWYEDLQEVLSSDENGGTYVSPPGNEEEESKIFTTLDPASL

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Query Match
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth arrest and DNA-damage-inducible protein GADD153 (DNA-damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P35638;
01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McBride O.W., Holbrook N.J.; "Isolation, characterization and chromosomal localization human GADD153 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92339899; PubMed=1339368;
Park J.S., Luethy J.D., Wang M.G., Fargnoli J., Fornace A.J. Jr.,
McBride O.W., Holbrook N.J.;
                                                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbitts T.H., Forster A., Larson R., Nathan P.;
"Fusion of the dominant negative transcription regulator CHOP with a novel gene FUS by translocation t(12;16) in malignant liposarcoma.";
Nat. Genet. 4:175-180(1993).
-i- FUNCTION: INHIBITS THE DNA-BINDING ACTIVITY OF C/EBP AND LAP BY FORMING HETERODIMERS THAT CANNOT BIND DNA.
-i- SUBUNIT: HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=93288139; PubMed=8510758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crozat A., Aman P., Mandahl N., Ron D.; "Fusion of CHOP to a novel RNA-binding protein in human myxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inducible transcript 3) (DDIT3) (C/EBP-homologous protein) (CHOP).
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                      Chromosomal translocation; Proto-oncogene.

DOMAIN 93 97 POLY-GLU.
                                                                                                                                                                                                                                                                                                                     Growth arrest; Nuclear protein; Transcription regulation; Repressor;
                                                                                                                                                                                                                                                                                                                                          SMART; SM00338; BRLZ;
                                                                                                                                                                                                                                                                                                                                                                                              MIM; 126337; -. MIM; 151900; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S62138; AAB27103.1; PIR; JC1169; JC1169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93350637; PubMed=7503811;
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                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S40706; AAB22646.1;
                                                                                                                                                                                                                                                                                                                                                                        InterPro;
1 MAAESLPFTLETVSSWELEAWYEDLQEVLSSDEIGGTYISSPGNEEEESKTFTTLDPASL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear. DISEASE: A FORM OF MYXOID LIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: SOME, TO BZIP PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: A FORM OF MYXOID LIPOSARCOMA IS CHARACTERIZED BY CHROMOSOMAL TRANSLOCATION T(12;16)(Q13;P11) THAT INVOLVES
                                                         85;
                                                                               Similarity
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19175 MW;
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                                                                               84.7%;
85.0%;
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                                                                                                                                                                                    LEUCINE-ZIPPER.
FGTLSS -> SDTVS (IN REF.
; 31905293FB1FBBE2 CRC64
                                                                               pred. No. 3.3e-34;
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                                                         Mismatches
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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1: sp_archea:
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508
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(without alignments)
695.069 Million cell updates/sec
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sp_virus:*
sp_vertebrate:*
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sp_archeap:*
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01-NOV-1996 (TrEMBLrel. 01,
                                        Q62804
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                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC013718; AAH13718.1; -
SEQUENCE 168 AA; 19190 MW; CC993B7957F43160 CRC64;
                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen C.H., Nusscnzweig A., Li G., Ling C.C.; "Cloning of rat GADD153 and its expression in submitted (AUG-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                      STRAIN-SPRAGUE DAWLEY; TISSUE-BRAIN;
Jin K.L., Chen J., Simon R.P., Graham S.H.;
submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U36994; AAA87944.1; -.
InterPro; IPR001871; bZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1995) to the EMBL; U30186; AAA73629.1; InterPro; IPR001871; bZIP.
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  Q9CYA4
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                                                                 AWLTEEPGPAEVTSTSQSPRSPDSSQSSMAQEEEEEDQG
                                                                                      AWLTEEPGPTEVTRTSQSPRSPDSSQSSMAQEEEEEEQG 99
                                                                                                                 MAAESLPFAFETVSSWELEAWYEDLQEVLSSDEIGGTYISSPGNEEEESKTFTTLDPASL 60
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Pred. No. 1.4e-42
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Sciurognathi; Muridae; Murinae; Rattus.
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Sciurognathi; Muridae; Murinae;
   PRT;
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01-OCT-2000
01-OCT-2000
01-JUN-2001
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
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Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mus musculus (Mouse).

Finkarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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InterPro; IPR000313; PWWP.
Pfam; PF00855; PWWP; 1.
SMART; SM00293; PWWP; 1.
                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
TDRM1 PROTEIN (UNKNOWN) (PROTEIN FOR MGC:6452).
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                           SEQUENCE FROM N.A. STRAIN=BALB/C; TIS Zhao Y., Chen W.,
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EMBL; AK017863; BAB30979.1; -
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
of novel gene related to thymus development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                 TISSUE=THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROWTH
                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%;
30.9%;
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17,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                 Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OAE1CF574DA1733C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.03;
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                                                                                                                                                                                                                                                                                                                                                                       update)
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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                   330
            Match
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18.9
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2: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1981.DAT: *
2: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1982.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1983.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1983.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1983.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1983.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1985.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1987.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1987.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1987.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1997.DAT: *
7: \SIDSI\gcgdata\hold-geneseq\geneseqp-embl\Aa1999.DAT: *
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Gapop 10.0 , Gapext 0.5
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508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAAESLPETLETVSSWELEA......RSPDSSQSSMAQEEEEEEQG
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       80
215
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322
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331
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  AAG32233
AAG32233
AAG32232
AAG365991
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AAG06990
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AAW80745
                                                                                                                                                                                                                                                                                                 ID
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               Human secreted pro
Mouse liver cancer
Arabidopsis thalia
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Arabidopsis
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	72	72	72	N			72.5	N.	•	7 3	73	73	73	73.5	73.5	74	75	75	75	75.5	75.5	75.5	76	77	77	78.5	78.5	80	80	80	80	87.5	88	88
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	480	309	301	1135	1065	686	905	868	969	932	117	117	117	438	361	1468	479	184	169	363	343	332	707	309	301	443	271	240	240	240	150	458	237	218
!	17	21	21	18	21	21	18	21	22	22	22	22	22	22	21	22	21	22	22	21	21	21	22	21	21	22	22	22	21	16	22	21	18	19
,	AARREDI 3	AAG19260	AAG19261	AAW31185	AAG46293	AAG46294	AAW31186	AAG46295	AA030116	ABB65256	AAU37501	AAU37274	AAU36840	ABB61455	AAY70948	ABB65329	AAY92242	AAM41613	AAM39827	AAG40820	AAG40821	AAG40822	AAM93718	AAG05798	AAG05799	ABG28288	S	ABB50263	99	\mathbf{a}		766	321	AAW80744
browity tarvae PM9			Arabidopsis thalla	Human pl60 polypep	Arabidopsis thalia	Arabidopsis thalia	Human p160 polypep	dopsis thall	Novel human secret	Drosophila melanog			Staphylococcus aur	Drosophila melanog	Mouse occyte-speci	0	cancer ass	polypeptid	an polypeptide	mays	mays protein	Zea mays protein f	Human polypentide.	Arabidopsis thalia	Arabidopsis thalla	Novel himan diagno	Drosophila melanog	oma-derived		henatoma de	hHDGF	agen binding	e hepato	Human liver cancer

ALIGNMENTS

AAG01619	1619
X H	AAG01619 standard; Protein; 80 AA.
X A	AAG01619;
Į,	06-OCT-2000 (first entry)
DE X	Human secreted protein, SEO ID NO: 5700
X	,
KΨ	Human; 5' EST; expressed sequence tag: secreted protein: CDNA isolation:
XX	
80	Homo saplens.
PN	EP1033401-A2.
X	
PD	06-SEP-2000.
×	
Ήď	21-FEB-2000; 2000EP-0200610.
×	
PR	26-FEB-1999; 99US-0122487.
ΡA	(GEST) GENSET.
×	
PI	Dumas Milne Edwards J, Duclert A, Giordano J;
DR	WPI; 2000-500381/45.
R	N-PSDB; AAC01625.
X	

XPTPT

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene'therapy and chromosome mapping procedures

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   AAW80745
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3'. untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW80745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW80745 standard; Protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID 5700; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1998 (first entry)
This represents the mouse liver cancer cell-derived growth factor (mHDGF). HDGF facilitates nuclear transfer. The invention provides
                                                Claim 17; Pages 17-18; 22pp; Japanese.
                                                                              New nucleus-transfer signal introducing human liver cancer cell-derived growth factor to nucleus - and new recombinant DNA, mutant and transformed E. Coli and animal cells
                                                                                                                                              WPI; 1998-535025/46.
N-PSDB; AAV55933.
                                                                                                                                                                                                                                                                  25-FEB-1997;
                                                                                                                                                                                                                                                                                                   08-SEP-1998.
                                                                                                                                                                                                                                                                                                                                  JP10234369-A.
                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleus-transfer signal peptide; HDGF-NLS; HDGF protein; mouse; human; liver cancer cell-derived growth factor; nuclear transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse liver cancer cell-derived growth factor (mHDGF).
                                                                                                                                                                                                 (SEKI ) SEKISUI CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AWLT-EEPGPTEVTRTSQSP 79
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                                                                                                                                                                                                                                  97JP-0040824.
                                                                                                                                                                                                                                                                  97JP-0040824
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 76..95
                                                                                                                                                                                                                                                                                                                                                                 /note= "the DNA sequence encoding the amino acids
    in this region are transposed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.1%;
83.8%;
                                                                                                                                                                                                     CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 80;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                               25 FEB-1999

05-MAR-1999

09-MAR-1999

23 MAR-1999

25-MAR-1999

06-APR-1999

06-APR-1999

01-APR-1999

16-APR-1999

17-APR-1999

21-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

25-MAY-1999

06-MAY-1999

06-MAY-1999

07-MAY-1999

07-MAY-1999

11-MAY-1999

11-MAY-1999

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11-MAY-1999

11-MAY-1999

11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleus-transfer signal peptides (mHDGF-NLS1, mHDGF-NLS2) of mHDGF and nucleus-transfer signal peptides (hHDGF-NLS1, hHDGF-NLS2) of human liver cancer cell-derived growth factor (hHDGF). A recombinant DNA molecule in which any of the DNA base sequences encoding the peptides is recombined to a vector, can be used to transform E. coli or other animal host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG32234 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG32234;
                                                                                                                                                                                                                                                                                                                                               25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 tpsepdsggppaeeeegeee 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 ssdeegklvidepakeknekgtlesgdheeedkeiaale-----gerhlpvevekns- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 SPRSPDSSQSSMAQEEEEEEQ 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 AA;
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                                                                                                                                    990S-0130449.
990S-0130510.
990S-0130891.
990S-0131449.
990S-0132048.
990S-0132407.
                                                                                       99US-0132484.
99US-0132485.
99US-0132486.
99US-0132487.
                                                                                                                                                                                                                                                                                        99US-0123180.
99US-0123548.
99US-0125788.
99US-0132863.
99US-0134216.
99US-0134219.
99US-0134219.
99US-0134221.
99US-0134370.
99US-0134768.
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99US-0130077.
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                                                                                                                                                                                                                                                         99US-0127462
                                                                                                                                                                                                                                                                  99US-0126264
99US-0126785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 19; Length 215; Pred. No. 0.027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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